

<110> ARES TRADING S.A.

&lt;120&gt; IL-8-LIKE PROTEINS

<130> P032741WO

<140> PCT/GB03/05621

<141> 2003-12-19

<150> GB 0229854.5

<151> 2002-12-20

<160> 24

<170> SeqWin99, version 1.02

<210> 1

<211> 126

<212> DNA

<213> Homo sapiens

<400> 1

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<210> 2

<211> 42

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<213> Homo sapiens

<400> 2

Met Ser Ala Gln His Gly Leu Val Ser Lys Phe Gly Leu Gly Leu Leu  
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Leu Leu Gly Asp Lys Tyr Phe Gln Arg His Glu Gln Ser Lys Pro His  
20 25 30

Gln Glu Glu Ile Asp Asn Leu His Ser Pro  
35 40

<210> 3

<211>      330

<212> DNA

<213> Homo sapiens

<400> 3

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aggcctcaaa	ctgccccaa	agcaggcaaa	ggtcagatgt	gtggagagag	gatggcgagg	180
atggcaagga	cggccaagga	gggtcgcccc	aggtgcctgg	accaggttt	gtcccgacc	240
ccgcacctg	gccacatgt	cttcttccc	catagcccca	ccccagcatc	ctggcaccag	300
tgggtcctg	gtggcactgg	ctggatgctg				330

<210> 4  
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<400> 4  
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 Cys Ser Pro Arg Gly Thr Leu Leu Glu Gly Pro Met Ser Ser Gly Phe  
 20 25 30  
 His Arg Phe Glu Val Glu Asn Leu Arg Pro Gln Thr Ala Pro Lys Ala  
 35 40 45  
 Gly Lys Gly Gln Met Cys Gly Glu Arg Met Ala Arg Met Ala Arg Thr  
 50 55 60  
 Ala Lys Glu Gly Arg Pro Arg Cys Leu Asp Pro Gly Leu Ser Arg Thr  
 65 70 75 80  
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 85 90 95  
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 ccccggggga ccctcctcga gggcccatg tcttctgggt tccatcgctt tgaggtagaa 240  
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 gcgaggatgg caaggacggc caaggagggt cgcccaggt gcctggacct aggtttgtcc 360  
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 Leu Leu Gly Asp Lys Tyr Phe Gln Arg His Glu Gln Ser Lys Pro His  
 20 25 30

Gln Glu Glu Ile Asp Asn Leu His Ser Pro Asp Leu Pro Thr Pro Gly  
           35                          40                          45

His Pro Val Thr Leu His Ser Leu Cys Phe Cys Ser Pro Arg Gly Thr  
       50                          55                          60

Leu Leu Glu Gly Pro Met Ser Ser Gly Phe His Arg Phe Glu Val Glu  
   65                          70                          75                          80

Asn Leu Arg Pro Gln Thr Ala Pro Lys Ala Gly Lys Gly Gln Met Cys  
                           85                          90                          95

Gly Glu Arg Met Ala Arg Met Ala Arg Thr Ala Lys Glu Gly Arg Pro  
                           100                          105                          110

Arg Cys Leu Asp Pro Gly Leu Ser Arg Thr Pro His Pro Gly Pro His  
           115                          120                          125

Val Phe Leu Pro His Ser Pro Thr Pro Ala Ser Trp His Gln Trp Ala  
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Pro Gly Gly Thr Gly Trp Met Leu  
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<210> 7  
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 aaaataaata tgttattcag tcagaaccac tggactataa gaagtatatt ccattctggt 180  
 ttttactggg ggaaaggatg ttgccacaag atgtcagtc atttattcat tcatatatcc 240  
 aatagatatt ttatgaccac ttccatgtgc caggagatgg ctaagatcct tggaagacag 300  
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Gln Thr Met Ala Phe Ser Ala Thr Lys Ile Asn Met Leu Phe Ser Gln  
       35                          40                          45

Asn His Trp Thr Ile Arg Ser Ile Phe His Ser Gly Phe Tyr Trp Gly  
       50                          55                          60

Lys Gly Cys Cys His Lys Met Ser Val His Leu Phe Ile His Ile Ser  
65 70 75 80

Asn Arg Tyr Phe Met Thr Thr Ser Met Cys Gln Glu Met Ala Lys Ile  
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Leu Gly Arg Gln Ile Lys Cys Tyr Leu Pro Thr Gln Ser Pro Val Arg  
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Glu Ser Gly Gly Lys Thr Ile Phe  
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<210> 9  
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aaaataaata tgttattcag tcagaaccac tggactataa gaagtatatt ccattctggt 180  
ttttactggg ggaaaggatg ttgccacaag atgtcagtc atttattcat tcatatatcc 240  
aatagatatt ttatgaccac ttccatgtgc caggagatgg ctaagatcct tggaagacag 300  
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<210> 10  
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<400> 10  
Asn Thr Glu Asn Asp Phe Tyr Glu Ile Cys Gly Asn Gln Ser His His  
1 5 10 15

His Asp Asn Ala Arg Ile Lys Lys Leu Val Asp Gly Leu Glu Phe Ser  
20 25 30

Gln Thr Met Ala Phe Ser Ala Thr Lys Ile Asn Met Leu Phe Ser Gln  
35 40 45

Asn His Trp Thr Ile Arg Ser Ile Phe His Ser Gly Phe Tyr Trp Gly  
50 55 60

Lys Gly Cys Cys His Lys Met Ser Val His Leu Phe Ile His Ile Ser  
65 70 75 80

Asn Arg Tyr Phe Met Thr Thr Ser Met Cys Gln Glu Met Ala Lys Ile  
85 90 95

Leu Gly Arg Gln Ile Lys Cys Tyr Leu Pro Thr Gln Ser Pro Val Arg  
100 105 110

Glu Ser Gly Gly Lys Thr Ile Phe  
115 120

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 ttattcattc atatatccaa tagatatattt atgaccactt ccatgtgccca ggagatggct 180  
 aagatccttg gaagacagat aaaatgctac ctaccaactc aaagtccagt tagggagtca 240  
 gggggtaaaa caatattcta gcaca 265

<210> 12  
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<400> 12  
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 Cys Cys His Lys Met Ser Val His Leu Phe Ile His Ile Ser Asn Arg  
 35 40 45  
 Tyr Phe Met Thr Thr Ser Met Cys Gln Glu Met Ala Lys Ile Leu Gly  
 50 55 60  
 Arg Gln Ile Lys Cys Tyr Leu Pro Thr Gln Ser Pro Val Arg Glu Ser  
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 Gly Gly Lys Thr Ile Phe  
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<210> 13  
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<400> 13  
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<210> 14  
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<400> 19  
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<210> 20  
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<210> 21  
<211> 18  
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<210> 22  
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<210> 23  
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<220>  
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<400> 23  
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<210> 24  
<211> 18  
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<213> Artificial Sequence

<220>  
<223> Primer T3

<400> 24  
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18